

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/723,164
Source: 1FWO
Date Processed by STIC: 11/18/04

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 11/18/2004

PATENT APPLICATION: US/10/723,164

TIME: 09:31:36

Input Set : A:\66783-142.TXT

Output Set: N:\CRF4\11182004\J723164.raw

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4 <110> APPLICANT: Targan, Stephan R.
5   Vasiliasauskas, Eric A.
6   Mow, William S.
7   Yang, Huiying
8   Fleshner, Phillip R.
9   Rotter, Jerome I.
11 <120> TITLE OF INVENTION: Methods of Assessing Crohn's Disease
12   Patient Phenotype by I2, OmpC and ASCA Serologic Response
16 <130> FILE REFERENCE: 66783-142
18 <140> CURRENT APPLICATION NUMBER: US 10/723,164
19 <141> CURRENT FILING DATE: 2003-11-26
21 <150> PRIOR APPLICATION NUMBER: US 10/413,501
22 <151> PRIOR FILING DATE: 2003-04-11
24 <160> NUMBER OF SEQ ID NOS: 22.
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 302
30 <212> TYPE: DNA
31 <213> ORGANISM: P. aeruginosa
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (2)...(301)
37 <400> SEQUENCE: 1
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39   Asp Leu Ala Ser Ala Val Gly Ile Gln Ser Gly Ser Ile Phe His
40   1         5         10        15
42 ttc aag agc aag gat gag ata ttg cgt gcc gtg atg gag gaa acc atc 97
43   Phe Lys Ser Lys Asp Glu Ile Leu Arg Ala Val Met Glu Glu Thr Ile
44   20        25        30
46 cat tac aac acc gcg atg atg cgc gct tca ctg gag gag gcg agc acg 145
47   His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Glu Ala Ser Thr
48   35        40        45
50 gtg cgc gaa cgc gtg ctg gcg ctg atc cgc tgc gag ttg cag tgc atc 193
51   Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile
52   50        55        60
54 atg ggc ggc agt ggc gag gcc atg gcg gtg ctg gtc tac gaa tgg cgc 241
55   Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg
56   65        70        75        80
58 tgc ctg tgc gcc gaa ggc cag gcg cac gtg ctg gcc ctg cgt gac gtg 289
59   Ser Leu Ser Ala Glu Gly Gln Ala His Val Leu Ala Leu Arg Asp Val
60   85        90        95
62 tat gag cag atc t 302
63 Tyr Glu Gln Ile

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68 <211> LENGTH: 100
69 <212> TYPE: PRT
70 <213> ORGANISM: P. aeruginosa
72 <400> SEQUENCE: 2
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74 1      5      10      15
75 Phe Lys Ser Lys Asp Glu Ile Leu Arg Ala Val Met Glu Glu Thr Ile
76      20      25      30
77 His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Glu Ala Ser Thr
78      35      40      45
79 Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile
80      50      55      60
81 Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg
82 65      70      75      80
83 Ser Leu Ser Ala Glu Gly Gln Ala His Val Leu Ala Leu Arg Asp Val
84      85      90      95
85 Tyr Glu Gln Ile
86      100
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90 <211> LENGTH: 494
91 <212> TYPE: DNA
92 <213> ORGANISM: Homo sapiens
94 <400> SEQUENCE: 3
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96 tggctgagtg ccagacatct gagaaggccc tgcctcggcg ccaggcctgt gcccgtggt 120
97 gtctggcccg cagcctccgc aagcaacttc actccatccc gccagctgca ccgggtgagg 180
98 ccaagagcgt gcatgccatg cccgggttca tctggctcat ccggagcctg tacgagatgc 240
99 aggaggagcg gctggctcgg aaggctgcac gtggcctgaa tggtgggcac ctcaagttga 300
100 cattttgcag tgtgggcccc actgagtgtg ctgccctggc ctttgtgctg cagcacctcc 360
101 ggcggcccggt ggccctgcag ctggactaca actctgtggg tgacattggc ctggagcagc 420
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103 aggtatgggg gagc
105 <210> SEQ ID NO: 4
106 <211> LENGTH: 494
107 <212> TYPE: DNA
108 <213> ORGANISM: Homo sapiens
110 <400> SEQUENCE: 4
111 gtcaccccat acctgaacag caatgccag taacactcac tacagagcct tgcagacacc 60
112 aaggcaaggc agcagctgct ccaggccaat gtcaccaca gagttgtagt ccagctgcag 120
113 ggccacgggc cgccggagggt gctgcagcac aaaggccagg gcagcacact cagtggggcc 180
114 cacactgcaa aatgtcaact tgagggtgcc aacattcagg ccacgtgcag ccttccgagc 240
115 cagccgctcc tctgcatct cgtacaggct ccggatgagc cagatgaacc cgggcatggc 300
116 atgcacgctc ttggcctcac ccggtgcagc tggcgggatg gagtggaagt gcttgccggag 360
117 gctgcggggc agacaccagc gggcacaggc ctggcgccgg agcagggcct tctcagatgt 420
118 ctggcactca gccagcaggc cccagtgtc ccgggacaac agccctgcc a ggaaggctgc 480
119 tgtgatctga aggt
121 <210> SEQ ID NO: 5

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122 <211> LENGTH: 540
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128 ctcttgaaat ccaatgggtct tttttcctta ctccattgcc taacattgtg gggtagaaat 120
129 aaagttcaaa gaccttcaga actggcccca gctcctccct cttcacctga tctccccaa 180
130 aaaactgcag gatagactct gaagcttacc tgagccacct caagctctgg tgatcaccca 240
131 aggcttcagc cagggcctgg gccccctcgt caccactct gttgcccag aatctgaaaa 300
132 ggccaaaaga gtcaacagac agtgtcagtg agtacctgat atgtgttcta gacatgaact 360
133 aacagtcctc ctccctctgc agtcccagcc agaggggcag gaccactcaa tcccagagt 420
134 gcctcactgg ggctcctggg cccagcaaag tggacctgcc tccatctttt gggtaggat 480
135 gccaaactta acccaagagt ttccagtggc ttacattac agacttagag aatagtagag 540
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139 <211> LENGTH: 540
140 <212> TYPE: DNA
141 <213> ORGANISM: Homo sapiens
143 <400> SEQUENCE: 6
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145 catcccaccc aaaagatgga ggcaggtcca ctttgctggg accaggagcc ccagtgggc 120
146 cactctggga ttgagtggc ctgcccctct ggctgggact gcagaggag gaggactgtt 180
147 agttcatgtc tagaacacat atcaggtact cactgacact gtctgttgac tcttttggc 240
148 ttttcagatt ctggggcaac agagtgggtg acgagggggc ccaggccctg gctgaagcct 300
149 tgggtgatca ccagagcttg aggtggctca ggtaagcttc agagtctatc ctgcagtttt 360
150 cttggggaga tcaggtgaag agggaggagc tggggccagt tctgaaggtc tttgaacttt 420
151 atttctaccc cacaatgtta ggcaatggag taaggaaaaa agaccattgg atttcaagag 480
152 aggacactcg agtctttctg ggtgacttgg aaatgtccct tgtcctctca gggttttgat 540
155 <210> SEQ ID NO: 7
156 <211> LENGTH: 541
157 <212> TYPE: DNA
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 7
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162 aatcagatcc ttcacatgca gaatcattct cactgaatgt cagaatcaga agggatcctc 120
163 aaaattctgc cattcctctc tcccgtcacc ccattttaca gatagaaaaa ctgaggttcg 180
164 gagagctaaa acaggcctgc ccaggggcct taccagactt ccaggatggg gtcattcctt 240
165 tcaaggggccc tgcaggaggg cttctgcccc taggtaggtg atgcagttat tggacaacct 300
166 ggaaaagaag atacaatggg gagcttcaag gattcttggg tttcctcttg aaactgtcca 360
167 gttaaagaga ctgcaggagt tagccagtct actgaagccc acctgtccct tagacacatc 420
168 ctgctcatgt ctgagattcc caatgagctc atcaacaaag gctcagtacc atcagtgaag 480
169 tgtaaccgtc tctcttccat tcactagatg agtttatcaa attaagtagc cactccctta 540
170 g 541
172 <210> SEQ ID NO: 8
173 <211> LENGTH: 541
174 <212> TYPE: DNA
175 <213> ORGANISM: Homo sapiens
177 <400> SEQUENCE: 8
178 ctaagggagt ggctacttaa tttgataaac tcatctagtg aatggaagag agacgggttac 60
179 atttactga tggtagtgag cctttgttga tgagctcatt ggaatctca gacatgagca 120

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180 ggatgtgtct aaggacagg tgggcttcag tagactggct aactcctgca gtctctttaa 180
181 ctggacagtt tcaagaggaa aaccaagaat ccttgaagct caccattgta tcttcttttc 240
182 caggttggtcc aataactgca tcacctacct aggggcagaa gccctcctgc agggcccttg 300
183 aaaggaatga caccatcctg gaagtctggt aaggccctg ggcaggcctg ttttagctct 360
184 ccgaacctca gtttttctat ctgtaaaatg ggtgacggg agagaggaat ggcagaattt 420
185 tgaggatccc ttctgattct gacattcagt gagaatgatt ctgcatgtga aggatctgat 480
186 tctctgtcta agaaagaagt ctttacctct ttaagtaggg agcaatgatt tcatttttaa 540
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190 <211> LENGTH: 1101
191 <212> TYPE: DNA
192 <213> ORGANISM: E. coli
194 <220> FEATURE:
195 <221> NAME/KEY: CDS
196 <222> LOCATION: (1)...(1101)
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201 1 5 10 15
203 ggc gca gca aac gct gct gaa gtt tac aac aaa gac ggc aac aaa tta 96
204 Gly Ala Ala Asn Ala Ala Glu Val Tyr Asn-Lys Asp Gly Asn Lys Leu
205 20 25 30
207 gat ctg tac ggt aaa gta gac ggc ctg cac tat ttc tct gac aac aaa 144
208 Asp Leu Tyr Gly Lys Val Asp Gly Leu His Tyr Phe Ser Asp Asn Lys
209 35 40 45
211 gat gta gat ggc gac cag acc tac atg cgt ctt ggc ttc aaa ggt gaa 192
212 Asp Val Asp Gly Asp Gln Thr Tyr Met Arg Leu Gly Phe Lys Gly Glu
213 50 55 60
215 act cag gtt act gac cag ctg acc ggt tac ggc cag tgg gaa tat cag 240
216 Thr Gln Val Thr Asp Gln Leu Thr Gly Tyr Gly Gln Trp Glu Tyr Gln
217 65 70 75 80
219 atc cag ggc aac agc gct gaa aac gaa aac aac tcc tgg acc cgt gtg 288
220 Ile Gln Gly Asn Ser Ala Glu Asn Glu Asn Asn Ser Trp Thr Arg Val
221 85 90 95
223 gca ttc gca ggt ctg aaa ttc cag gat gtg ggt tct ttc gac tac ggt 336
224 Ala Phe Ala Gly Leu Lys Phe Gln Asp Val Gly Ser Phe Asp Tyr Gly
225 100 105 110
227 cgt aac tac ggc gtt gtt tat gac gta act tcc tgg acc gac gta ctg 384
228 Arg Asn Tyr Gly Val Val Tyr Asp Val Thr Ser Trp Thr Asp Val Leu
229 115 120 125
231 cca gaa ttc ggt ggt gac acc tac ggt tct gac aac ttc atg cag cag 432
232 Pro Glu Phe Gly Gly Asp Thr Tyr Gly Ser Asp Asn Phe Met Gln Gln
233 130 135 140
235 cgt ggt aac ggc ttc gcg acc tac cgt aac act gac ttc ttc ggt ctg 480
236 Arg Gly Asn Gly Phe Ala Thr Tyr Arg Asn Thr Asp Phe Phe Gly Leu
237 145 150 155 160
239 gtt gac ggc ctg aac ttt gct gtt cag tac cag ggt aaa aac ggc aac 528
240 Val Asp Gly Leu Asn Phe Ala Val Gln Tyr Gln Gly Lys Asn Gly Asn
241 165 170 175

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243 cca tct ggt gaa ggc ttt act agt ggc gta act aac aac ggt cgt gac 576
244 Pro Ser Gly Glu Gly Phe Thr Ser Gly Val Thr Asn Asn Gly Arg Asp
245      180      185      190
247 gca ctg cgt caa aac ggc gac ggc gtc ggc ggt tct atc act tat gat 624
248 Ala Leu Arg Gln Asn Gly Asp Gly Val Gly Gly Ser Ile Thr Tyr Asp
249      195      200      205
251 tac gaa ggt ttc ggt atc ggt ggt gcg atc tcc agc tcc aaa cgt act 672
252 Tyr Glu Gly Phe Gly Ile Gly Gly Ala Ile Ser Ser Ser Lys Arg Thr
253      210      215      220
255 gat gct cag aac acc gct gct tac atc ggt aac ggc gac cgt gct gaa 720
256 Asp Ala Gln Asn Thr Ala Ala Tyr Ile Gly Asn Gly Asp Arg Ala Glu
257 225      230      235      240
259 acc tac act ggt ggt ctg aaa tac gac gct aac aac atc tac ctg gct 768
260 Thr Tyr Thr Gly Gly Leu Lys Tyr Asp Ala Asn Asn Ile Tyr Leu Ala
261      245      250      255
263 gct cag tac acc cag acc tac aac gca act cgc gta ggt tcc ctg ggt 816
264 Ala Gln Tyr Thr Gln Thr Tyr Asn Ala Thr Arg Val Gly Ser Leu Gly
265      260      265      270
267 tgg gcg aac aaa gca cag aac ttc gaa gct gtt gct cag tac cag ttc 864
268 Trp Ala Asn Lys Ala Gln Asn Phe Glu Ala Val Ala Gln Tyr Gln Phe
269      275      280      285
271 gac ttc ggt ctg cgt ccg tcc ctg gct tac ctg cag tct aaa ggt aaa 912
272 Asp Phe Gly Leu Arg Pro Ser Leu Ala Tyr Leu Gln Ser Lys Gly Lys
273      290      295      300
275 aac ctg ggt cgt ggc tac gac gac gaa gat atc ctg aaa tat gtt gat 960
276 Asn Leu Gly Arg Gly Tyr Asp Asp Glu Asp Ile Leu Lys Tyr Val Asp
277 305      310      315      320
279 gtt ggt gct acc tac tac ttc aac aaa aac atg tcc acc tac gtt gac 1008
280 Val Gly Ala Thr Tyr Tyr Phe Asn Lys Asn Met Ser Thr Tyr Val Asp
281      325      330      335
283 tac aaa atc aac ctg ctg gac gac aac cag ttc act cgt gac gct ggc 1056
284 Tyr Lys Ile Asn Leu Leu Asp Asp Asn Gln Phe Thr Arg Asp Ala Gly
285      340      345      350
287 atc aac act gat aac atc gta gct ctg ggt ctg gtt tac cag ttc 1101
288 Ile Asn Thr Asp Asn Ile Val Ala Leu Gly Leu Val Tyr Gln Phe
289      355      360      365
293 <210> SEQ ID NO: 10
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295 <212> TYPE: PRT
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298 <400> SEQUENCE: 10
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301 Gly Ala Ala Asn Ala Ala Glu Val Tyr Asn Lys Asp Gly Asn Lys Leu
302      20      25      30
303 Asp Leu Tyr Gly Lys Val Asp Gly Leu His Tyr Phe Ser Asp Asn Lys
304      35      40      45
305 Asp Val Asp Gly Asp Gln Thr Tyr Met Arg Leu Gly Phe Lys Gly Glu
306      50      55      60

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